AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph on page 1, line 2 as follows:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of application no. 09/229,911 filed January 13, 1999, which is a divisional of application no. 08/651,136 filed May 21, 1996, which is a continuation of PCT/DK96/00105 filed March 18, 1996, and claims priority under 35 U.S.C. 119 of Danish application nos. 0272/95, 0888/95, 0887/95, 0886/95, 0885/95 and 0137/96 filed on March 17, 1995, August 8, 1995, August 8, 1995, August 8, 1995, August 8, 1995, and February 12, 1996, respectively~~, the contents of which are fully incorporated herein by reference~~.

Please amend the paragraph from page 6, line 32 – page 7, line 2 as follows:

Figure 1 is an alignment of the deduced encoded amino acid sequences of *Acremonium sp. (I)* (SEQ ID NO: 8), *Volutella colletotrichoides* (SEQ ID NO: 22), *Crinipellis scabella* (SEQ ID NO: 16), *Acremonium sp. (II)* (SEQ ID NO: 10), *Myceliophthora thermophila* (SEQ ID NO: 2), *Thielavia terrestris* (SEQ ID NO: 12), *Macrophomina phaseolina* (SEQ ID NO: 14). The Pileup program (Feng and Doolittle, 1987) (GCG package, version 8.0) was used to create the best alignment. Identical residues in at least four sequences (boxed) are indicated around the corresponding amino acids.

Please amend the paragraph on page 7, lines 27-28 as follows:

Figure 3 is an alignment of the deduced partial amino acid sequences derived from a selection of 26 of the 46 microorganisms described in Example 5 (SEQ ID NOS: 40, 30, 38, 74, 64, 32, 52, 62, 66, 28, 34, 68, 76, 72, 46, 54, 42, 36, 48, 44, 78, 58, 50, 60, and 56).

Please amend the paragraph on page 19, lines 7-18 as follows:

The homology referred to in i) above is determined as the degree of identity between the two sequences indicating a derivation of the first sequence from the second. The homology may suitably be determined by means of computer programs known in the art such as GAP provided in the GCG program package (Needleman, S.B. and Wunsch, C.D., *Journal of*

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Molecular Biology, 48: 443-453, 1970). Using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the DNA sequence exhibits a degree of identity preferably of at least 60%, more preferably at least 65%, more preferably at least 70%, even more preferably at least 80%, especially at least 90%, with the coding region of the DNA sequence of SEQ ID NO: ~~1, 4, 6, 8, 10, 12, or 16,~~ 1, 7, 9, 11, 13, 15, or 21, respectively, or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae*, DSM 9770, DSM 10082, DSM 10080, DSM 10081, *Escherichia coli*, DSM 10512, DSM 10511, DSM 10571, or DSM 10576, respectively.

Please amend the paragraph on page 67, lines 1-3 as follows:

~~DSC~~ Differential scanning calometry ("DSC") was done at neutral pH (7.0) using a MicroCalc Inc. MC calorimeter with a constant scan rate and raising the temperature from 20 to 90°C at a rate of 90° per hour.

Please amend the paragraph on page 75, lines 21-22 as follows:

The cDNA encoding the endoglucanase from *M. phaseolina* (SEQ ID NO: 13~~-23~~) is cloned into pYES2.0 as a BstX I/Not I fragment and the resulting plasmid is named pC1C477.

Please amend the paragraph on page 77, lines 4-6 as follows:

The DNA sequence of the cDNA encoding the endoglucanase from *Acremonium sp.* is of SEQ ID NO: 9~~-6~~ and the corresponding amino acid sequence is of SEQ ID NO: 10~~-7~~. The cDNA is obtainable from the plasmid in DSM 10080.

Please amend the paragraph on page 89, lines 6-7 as follows:

2. NIH Data Base (Entrez, version spring 1996) available on the internet ~~World Wide Web: (http://www3.ncbi.nlm.nih.gov/htbin/ef/entrezTAX)~~.

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